PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/762,568

DATE: 02/26/2001
TIME: 17:27:52

Input Set : A:\Cpg.pto
Output Set: N:\CRF3\02262001\I762568.raw

Does Not Comply
Corrected Diskette Needed
See pp 2, 3

```
      3 <110> APPLICANT: Nippon Institute for Biological Science
      5 <120> TITLE OF INVENTION: novel plasmid vector
      7 <130> FILE REFERENCE: PCTF0001-0
C-->  9 <140> CURRENT APPLICATION NUMBER: US/09/762,568
C-->  9 <141> CURRENT FILING DATE: 2001-02-06
      9 <150> PRIOR APPLICATION NUMBER: JP, Japanese Patent Application No. Hei 11-158351
W--> 10 <151> PRIOR FILING DATE: 1999-6-4
     12 <160> NUMBER OF SEQ ID NOS: 13
     14 <210> SEQ ID NO: 1
     15 <211> LENGTH: 31
     16 <212> TYPE: DNA
     17 <213> ORGANISM: Artificial Sequence
     19 <220> FEATURE:
     20 <223> OTHER INFORMATION: Designed PCR primer including 3' region of U3 and VspI restriction
enzyme
     21       site to multiply RSV LTR.
     23 <400> SEQUENCE: 1
     24 ggcattaatg tagtcttatg caatactcct g 31
     26 <210> SEQ ID NO: 2
     27 <211> LENGTH: 40
     28 <212> TYPE: DNA
     29 <213> ORGANISM: Artificial Sequence
     31 <220> FEATURE:
     32 <223> OTHER INFORMATION: Designed PCR primer including 5' non coding region of p19 gene, HincII,
     33       EcoRV and BglII restriction enzyme site to multiply RSV LTR and down stream
     34       region of LTR.
     36 <400> SEQUENCE: 2
     37 gttaacgata tcagatctgc ttgatccacc gggcgaccag 40
     39 <210> SEQ ID NO: 3
     40 <211> LENGTH: 36
     41 <212> TYPE: DNA
     42 <213> ORGANISM: Artificial Sequence
     44 <220> FEATURE:
     45 <223> OTHER INFORMATION: Designed PCR primer including 5' region of RSV integrase gene and BamHI
     46       restriction enzyme site to multiply RSV integrase gene.
     48 <400> SEQUENCE: 3
     49 ttggatccat gcccttgaga gaggctaaag atcttc 36
     51 <210> SEQ ID NO: 4
     52 <211> LENGTH: 33
     53 <212> TYPE: DNA
     54 <213> ORGANISM: Artificial Sequence
     56 <220> FEATURE:
     57 <223> OTHER INFORMATION: Designed PCR primer including 3' region of RSV integrase gene, polyA
     58       signal to multiply RSV integrase gene.
     60 <400> SEQUENCE: 4
     61 tttattttaa ctctcgttgg cagcaagggt gtc 33
     63 <210> SEQ ID NO: 5
     64 <211> LENGTH: 29
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65 <212> TYPE: DNA
66 <213> ORGANISM: Artificial Sequence
68 <220> FEATURE:
69 <223> OTHER INFORMATION: Designed PCR primer including 5' region of U5 and VspI restriction enzyme
70 site to multiply RSV LTR.
72 <400> SEQUENCE: 5
73 ggcattaatg aagccttctg cttcattca 29
75 <210> SEQ ID NO: 6
76 <211> LENGTH: 51
77 <212> TYPE: DNA
78 <213> ORGANISM: Artificial Sequence
80 <220> FEATURE:
81 <223> OTHER INFORMATION: Designed PCR primer including 3' region of RSV integrase gene, polyA
82 signal, nuclear localization signal of SV40 large T antigen to multiply RSV
83 integrase gene.
85 <400> SEQUENCE: 6
86 tttattttaa accttcctct tcttcttagg actctcgttg gcagcaaggg t 51
88 <210> SEQ ID NO: 7
89 <211> LENGTH: 858
90 <212> TYPE: DNA
91 <213> ORGANISM: Rous sarcoma virus
93 <220> FEATURE:
W--> 94 <221> NAME/KEY: TATA_signal
95 <222> LOCATION: (84)...(90)
W--> 96 <221> NAME/KEY: polyA_signal
97 <222> LOCATION: (107)...(112)
W--> 98 <221> NAME/KEY: TATA_signal
99 <222> LOCATION: (431)...(437)
W--> 100 <221> NAME/KEY: polyA_signal
101 <222> LOCATION: (454)...(459)

features misspelled:
TATA_signal
insert underscore between words

102 <223> OTHER INFORMATION: A part of circular form of RSV DNA, tandem repeat LTRs and adjacent non
103 coding region.
105 <400> SEQUENCE: 7
106 acgatcgtgc cttattagga aggcaacaga cgggtctaac acggattgga cgaaccactg 60
107 aattccgcat tgcggagata ttgtatttaa gtgcctagct cgatacaata aacgccattt 120
108 taccattcac cacattggtg tgcacctggg ttgatggctg gaccgttgat tccctgacga 180
109 ctacgagcac atgcatgaag cagaaggctt cattaatgta gtcttatgca atactcctgt 240
110 agtcttgcaa catgcttatg taacgatgag ttagcaacat gccttacaag gagagaaaag 300
111 gcaccgtgca cgacgattgg tggaagtaag gtggtatgat cgtaggtacg atcgtgcctt 360
112 attaggaagg caacagacgg gtctaacacg gattggacga accactgaat tccgcattgc 420
113 ggagatattg tatttaagtg cctagctcga tacaataaac gccattttac cattcaccac 480
114 attggtgtgc acctgggttg atggctggac cgttgattcc ctgacgacta cgagcacatg 540
115 catgaagcag aaggcttcat ttggtgaccc cgacgtgatc gttagggaat agtggtcggc 600
116 cacagacggc gtggcgatcc tgccctcatc cgtctcgctt attcggggag cggacgatga 660
117 ccctagtaga gggggctgcg gcttaggagg gcagaagctg agtggcgtcg gagggagctc 720
118 tactgcaggg agcccagata ccctaccgag aactcagaga gtcgttggaa gacgggaaga 780
119 aagcccgacg actgagcggt ccaccccagg cgtgattccg gttgctctgc gtgaccctgg 840
120 tcgcccggtg gatcaagc 858
122 <210> SEQ ID NO: 8

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123 <211> LENGTH: 972
124 <212> TYPE: DNA
125 <213> ORGANISM: Rous sarcoma virus
127 <220> FEATURE:
128 <221> NAME/KEY: CDS
129 <222> LOCATION: 1...972
131 <221> NAME/KEY: CDS
132 <222> LOCATION: 1...858
135 <400> SEQUENCE: 8

? Which response for CDS?
No CDS shown.

136 cccttgagag aggctaaaga tcttcatacc gctctccata ttggaccccg cgcgctatcc 60
137 aaagcgtgta atatatctat gcagcaggct agggaggttg ttcagacctg cccgcattgt 120
138 aattcagccc ctgcgttgga ggccggagta aaccctaggg gtttgggacc cctacagata 180
139 tggcagacag actttacgct tgagcctaga atggcccccc gttcctggct cgctgttact 240
140 gtggacaccg cctcatcagc gatagtcgta actcagcatg gccgtgtcac atcggttgct 300
141 gtacaacatc attgggccac ggctatcgcc gttttgggaa gaccaaaggc cataaaaaca 360
142 gataacgggt cctgcttcac gtctaaatcc acgcgagagt ggctcgcgag atgggggata 420
143 gcacacacca ccgggattcc gggtaattcc cagggtcaag ctatggtaga gcgggccaac 480
144 cggctcctga aagataggat ccgtgtgctt gcggaggggg acggctttat gaaaagaatc 540
145 cccaccagca aacaggggga actattagcc aaggcaatgt atgccctcaa tcactttgag 600
146 cgtggtgaaa acacgaaaac accgatacaa aaacactgga gacctaccgt tcttacagaa 660
147 ggacccccgg ttaaaatacg aatagagaca ggggagtggg aaaaaggatg gaacgtgctg 720
148 gtctggggac gaggttatgc cgctgtgaaa aacagggaca ctgataaggt tatttgggta 780
149 ccctctcgaa aagttaaacc ggacatcacc caaaaggatg aggtgactaa gaaagatgag 840
150 gcgagccctc tttttgcagg catttctgac tggataccct ggggagacaa gcaagaagga 900
151 ctccaaggag aaaccgctag caacaagcaa gaaagacccg gagaagacac ccttgctgcc 960
152 aacgagagtt aa 972
154 <210> SEQ ID NO: 9
155 <211> LENGTH: 21
156 <212> TYPE: DNA
157 <213> ORGANISM: Artificial Sequence
W--> 158 <220> FEATURE:
159 <223> OTHER INFORMATION: Designed PCR primer including 5' region of GFP gene and a part ofNheI
160 restriction enzyme site to multiply GFP gene.
162 <400> SEQUENCE: 9
163 ctagcgctac cggtcgccac c 21
165 <210> SEQ ID NO: 10
166 <211> LENGTH: 20
167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial Sequence
W--> 169 <220> FEATURE:
170 <223> OTHER INFORMATION: Designed PCR primer including antisense sequence of GFP ORF to multiply
a
171 part of GFP gene.
173 <400> SEQUENCE: 10
174 gttgccgtcc tccttgaagt 20
176 <210> SEQ ID NO: 11
177 <211> LENGTH: 21
178 <212> TYPE: DNA
179 <213> ORGANISM: Artificial Sequence
W--> 180 <220> FEATURE:

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181 <223> OTHER INFORMATION: Designed PCR primer including U5 region LTR sequence to
182 multiply a part of integrated plasmid vecter.
184 <400> SEQUENCE: 11
185 ttggtgtgca cctgggttga t 21
187 <210> SEQ ID NO: 12
188 <211> LENGTH: 36
189 <212> TYPE: DNA
190 <213> ORGANISM: Artificial Sequence
W--> 191 **<220> FEATURE:**
192 <223> OTHER INFORMATION: Designed PCR primer including 5' end of GFP ORF sequence to
193 multiply a part of GFP gene.
195 <400> SEQUENCE: 12
196 atggtgagca agggcgagga gctgttcacc ggggtg 36
198 <210> SEQ ID NO: 13
199 <211> LENGTH: 20
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
W--> 202 **<220> FEATURE:**
203 <223> OTHER INFORMATION: Designed PCR primer including a part of GFP ORF sequence to
204 multiply a part of GFP gene.
206 <400> SEQUENCE: 13
207 gtcgagctgg acggcgacgt 20

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:10 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:94 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:96 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:98 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:100 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:158 M:283 W: Missing Blank Line separator, <220> field identifier
L:169 M:283 W: Missing Blank Line separator, <220> field identifier
L:180 M:283 W: Missing Blank Line separator, <220> field identifier
L:191 M:283 W: Missing Blank Line separator, <220> field identifier
L:202 M:283 W: Missing Blank Line separator, <220> field identifier